

SEQUENCE LISTING

<110> DIVERSA CORPORATION
 BARTON, Nelson R.
 O'DONOGHUE, Eileen
 SHORT, Ryan
 FREY, Gerhard
 WEINER, David
 ROBERTSON, Dan E.
 BRIGGS, Steven
 ZORNER, Paul

<120> CHIMERIC CANNULAE PROTEINS, NUCLEIC ACIDS ENCODING
 THEM AND METHODS FOR MAKING AND USING THEM

<130> 564462006845

<140> Not Yet Assigned

<141> Concurrently Herewith

<150> 60/556,393

<151> 2004-03-24

<150> 60/605,192

<151> 2004-08-27

<160> 12

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 624

<212> DNA

<213> *Pyrodictium abyssi*

<400> 1

gtgaagtaca	caaccctagc	tatagcgggt	attattgcct	cggctgccgc	cctcgccctc	60
ctagcaggct	tcgccaccac	ccagagcccc	ctcaacagct	tctacgccac	cggtacagca	120
caggcagtaa	gcgagccaat	agacgtagaa	agccacctcg	gcagcataac	ccccgcagcc	180
ggcgcacagg	gcagtgacga	cataggttac	gcaatagtgt	ggataaagga	ccagggtcaat	240
gatgtaaagc	tgaagggtgac	cctgcgtaac	gctgagcagc	taaagcccta	cttcaagtac	300
ctacagatac	agataacaag	cggctatgag	acgaacagca	cagctctagg	caacttcagc	360
gagaccaagg	ctgtgataag	cctcgacaac	cccagcgccg	tgatagtact	agacaaggag	420
gatatagcag	tgctctatcc	ggacaagacc	ggttacacaa	acacttcgat	atgggtaccc	480
ggtgaacctg	acaagataat	tgtctacaac	gagacaaagc	cagtagctat	actgaacttc	540
aaggccttct	acgaggctaa	ggagggtatg	ctattcgaca	gcctgccagt	gatattcaac	600
ttccagggtgc	tacaagtagg	ctaa				624

<210> 2

<211> 207

<212> PRT

<213> *Pyrodictium abyssi*

<400> 2

Val	Lys	Tyr	Thr	Thr	Leu	Ala	Ile	Ala	Gly	Ile	Ile	Ala	Ser	Ala	Ala
1				5					10					15	
Ala	Leu	Ala	Leu	Leu	Ala	Gly	Phe	Ala	Thr	Thr	Gln	Ser	Pro	Leu	Asn
			20				25						30		
Ser	Phe	Tyr	Ala	Thr	Gly	Thr	Ala	Gln	Ala	Val	Ser	Glu	Pro	Ile	Asp
		35				40					45				
Val	Glu	Ser	His	Leu	Gly	Ser	Ile	Thr	Pro	Ala	Ala	Gly	Ala	Gln	Gly
	50					55					60				
Ser	Asp	Asp	Ile	Gly	Tyr	Ala	Ile	Val	Trp	Ile	Lys	Asp	Gln	Val	Asn
65				70					75					80	

Asp Val Lys Leu Lys Val Thr Leu Arg Asn Ala Glu Gln Leu Lys Pro
 85 90 95
 Tyr Phe Lys Tyr Leu Gln Ile Gln Ile Thr Ser Gly Tyr Glu Thr Asn
 100 105 110
 Ser Thr Ala Leu Gly Asn Phe Ser Glu Thr Lys Ala Val Ile Ser Leu
 115 120 125
 Asp Asn Pro Ser Ala Val Ile Val Leu Asp Lys Glu Asp Ile Ala Val
 130 135 140
 Leu Tyr Pro Asp Lys Thr Gly Tyr Thr Asn Thr Ser Ile Trp Val Pro
 145 150 155 160
 Gly Glu Pro Asp Lys Ile Ile Val Tyr Asn Glu Thr Lys Pro Val Ala
 165 170 175
 Ile Leu Asn Phe Lys Ala Phe Tyr Glu Ala Lys Glu Gly Met Leu Phe
 180 185 190
 Asp Ser Leu Pro Val Ile Phe Asn Phe Gln Val Leu Gln Val Gly
 195 200 205

<210> 3

<211> 513

<212> DNA

<213> Pyrodictium abyssi

<400> 3

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ctagcaggct	tcgccaccac	ccagagcccg	ctcaacagct	tctacgccac	cggcacagca	120
gccgcaacaa	gcgagccaat	agacgtagag	agccacctca	gcagcatagc	ccctgctgct	180
ggcgcacagg	gcagccagga	cataggctac	ttcaacgtga	ccgccaagga	tcaagtgaac	240
gtgacaaaga	taaaggtgac	cctggctaac	gctgagcagc	taaagcccta	cttcaagtac	300
ctacagatag	tgctaaagag	cgaggtagct	gacgagatca	aggccgtaat	aagcatagac	360
aagcctagcg	ccgtcataat	actagacagc	caggacttcg	acagcaacaa	cagagcaaag	420
ataagcgcca	ctgcctacta	cgaggctaag	gagggcatgc	tattcgacag	cctaccgcta	480
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<210> 4

<211> 170

<212> PRT

<213> Pyrodictium abyssi

<400> 4

Val Lys Pro Thr Ala Leu Ala Leu Ala Gly Ile Ile Ala Ser Ala Ala	1	5	10	15
Asp Leu Ala Leu Leu Ala Gly Phe Ala Thr Thr Gln Ser Pro Leu Asn	20	25	30	
Ser Phe Tyr Ala Thr Gly Thr Ala Ala Ala Thr Ser Glu Pro Ile Asp	35	40	45	
Val Glu Ser His Leu Ser Ser Ile Ala Pro Ala Ala Gly Ala Gln Gly	50	55	60	
Ser Gln Asp Ile Gly Tyr Phe Asn Val Thr Ala Lys Asp Gln Val Asn	65	70	75	80
Val Thr Lys Ile Lys Val Thr Leu Ala Asn Ala Glu Gln Leu Lys Pro	85	90	95	
Tyr Phe Lys Tyr Leu Gln Ile Val Leu Lys Ser Glu Val Ala Asp Glu	100	105	110	
Ile Lys Ala Val Ile Ser Ile Asp Lys Pro Ser Ala Val Ile Ile Leu	115	120	125	
Asp Ser Gln Asp Phe Asp Ser Asn Asn Arg Ala Lys Ile Ser Ala Thr	130	135	140	
Ala Tyr Tyr Glu Ala Lys Glu Gly Met Leu Phe Asp Ser Leu Pro Leu	145	150	155	160
Ile Phe Asn Ile Gln Val Leu Ser Val Ser	165	170		

<210> 5

<211> 537

<212> DNA

<213> *Pyrodictium abyssi*

<400> 5

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ctagcaggct tcgccacgac ccagagcccg ctaagcagct tctacgccac cggcacagca      120
caagcagtaa gcgagccaat agacgtagag agccacctag acaacacccat agcccctgct      180
gccggtgcac agggctacaa ggacatgggc tacattaaga taactaacca gtcaaaagtt      240
aatgtaataa agctgaaggt gactctcgct aacgccgagc agctaaagcc ctacttcgac      300
tacctacagc tagtactcac aagcaacgcc actggcaccg acatgggttaa ggctgtgcta      360
agcctcgaga agcctagcgc agtcataata ctagacaacg atgactacga tagcactaac      420
aagatacagc taaaggtaga agcctactat gaggctaagg agggcatgct attcgacagc      480
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<210> 6

<211> 178

<212> PRT

<213> *Pyrodictium abyssi*

<400> 6

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Met Arg Tyr Thr Thr Leu Ala Leu Ala Gly Ile Val Ala Ser Ala Ala
 1           5           10           15
Ala Leu Ala Leu Leu Ala Gly Phe Ala Thr Thr Gln Ser Pro Leu Ser
      20           25           30
Ser Phe Tyr Ala Thr Gly Thr Ala Gln Ala Val Ser Glu Pro Ile Asp
      35           40           45
Val Glu Ser His Leu Asp Asn Thr Ile Ala Pro Ala Ala Gly Ala Gln
      50           55           60
Gly Tyr Lys Asp Met Gly Tyr Ile Lys Ile Thr Asn Gln Ser Lys Val
      65           70           75           80
Asn Val Ile Lys Leu Lys Val Thr Leu Ala Asn Ala Glu Gln Leu Lys
      85           90           95
Pro Tyr Phe Asp Tyr Leu Gln Leu Val Leu Thr Ser Asn Ala Thr Gly
      100          105          110
Thr Asp Met Val Lys Ala Val Leu Ser Leu Glu Lys Pro Ser Ala Val
      115          120          125
Ile Ile Leu Asp Asn Asp Asp Tyr Asp Ser Thr Asn Lys Ile Gln Leu
      130          135          140
Lys Val Glu Ala Tyr Tyr Glu Ala Lys Glu Gly Met Leu Phe Asp Ser
      145          150          155          160
Leu Pro Val Ile Leu Asn Phe Gln Val Leu Ser Ala Ala Cys Ser Pro
      165          170          175
Leu Trp

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<210> 7

<211> 395

<212> DNA

<213> *Pyrodictium abyssi*

<400> 7

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atatatgcgc acaatgacgt gaacataaca aagctaaagg tcacgcttgc taacgctgca      180
cagctaagac catacttcaa gtacctgata ataaagctag taagcctgga cagcaacggc      240
aacgagtccg aggaaaaggg catgataact ctatggaagc cttacgccgt gataatacta      300
gaccatgaag atttcaacaa cgacatcgac aatgacggca acaatgacgc caagataagg      360
gttgtagcct actatgaggg taaggagggt atgct      395

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<210> 8

<211> 131

<212> PRT

<213> *Pyrodictium abyssi*

<400> 8

Ser Phe Tyr Ala Thr Gly Thr Ala Gln Ala Val Ser Glu Pro Ile Asp
 1 5 10 15
 Val Val Ser Ser Leu Gly Thr Leu Asn Thr Ala Ala Gly Ala Gln Gly
 20 25 30
 Lys Gln Thr Leu Gly Asp Ile Thr Ile Tyr Ala His Asn Asp Val Asn
 35 40 45
 Ile Thr Lys Leu Lys Val Thr Leu Ala Asn Ala Ala Gln Leu Arg Pro
 50 55 60
 Tyr Phe Lys Tyr Leu Ile Ile Lys Leu Val Ser Leu Asp Ser Asn Gly
 65 70 75 80
 Asn Glu Ser Glu Glu Lys Gly Met Ile Thr Leu Trp Lys Pro Tyr Ala
 85 90 95
 Val Ile Ile Leu Asp His Glu Asp Phe Asn Asn Asp Ile Asp Asn Asp
 100 105 110
 Gly Asn Asn Asp Ala Lys Ile Arg Val Val Ala Tyr Tyr Glu Ala Lys
 115 120 125
 Glu Gly Met
 130

<210> 9

<211> 372

<212> DNA

<213> Pyrodictium abyssi

<400> 9

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 cttaacacgg ccatagcccc tgctgccggc gccaggggca gcgtgggcat aggcagcata 120
 acaatagaga acaagactga cgtgaacgtt gtgaagctga agataaccct cgccaacgct 180
 gagcagctaa agccctactt cgactaccta cagatagtgc taaagagcgt tgacagcaac 240
 gagatcaagg ctgtgctaag cctcgagaag cccagcgcag tcataatact ggacaacgag 300
 gacttcagg gcggcgacaa ccagtgccag atagacgcca ccgcctacta cgaggctaag 360
 gagggtatgc ta 372

<210> 10

<211> 124

<212> PRT

<213> Pyrodictium abyssi

<400> 10

Ser Phe Tyr Ala Thr Gly Thr Ala Glu Ala Thr Ser Glu Pro Ile Asp
 1 5 10 15
 Val Val Ser Asn Leu Asn Thr Ala Ile Ala Pro Ala Ala Gly Ala Gln
 20 25 30
 Gly Ser Val Gly Ile Gly Ser Ile Thr Ile Glu Asn Lys Thr Asp Val
 35 40 45
 Asn Val Val Lys Leu Lys Ile Thr Leu Ala Asn Ala Glu Gln Leu Lys
 50 55 60
 Pro Tyr Phe Asp Tyr Leu Gln Ile Val Leu Lys Ser Val Asp Ser Asn
 65 70 75 80
 Glu Ile Lys Ala Val Leu Ser Leu Glu Lys Pro Ser Ala Val Ile Ile
 85 90 95
 Leu Asp Asn Glu Asp Phe Gln Gly Gly Asp Asn Gln Cys Gln Ile Asp
 100 105 110
 Ala Thr Ala Tyr Tyr Glu Ala Lys Glu Gly Met Leu
 115 120

<210> 11

<211> 448

<212> DNA

<213> Artificial Sequence

<220>

<223> consensus sequence

<400> 11

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cccagagccc	ctacagcttc	tacgccaccg	gcacagcaca	ggcagtaagc	gagccaatag	120
acgtagaaag	ccacctcaca	catagcccct	gctgocggcg	cacagggcag	caggacatag	180
gctacataaa	ataacaagat	agtgaacgta	taaagctgaa	ggtgaccctg	ctaacgctga	240
gcagctaaag	ccctacttca	agtacctaca	gatagtgcata	aaagcgacag	caggcacacg	300
agaaggcgtg	ataagcctcg	agaagcctag	cgccgtcata	atactagaca	acgaggactt	360
cgaagcaca	cagaaagaga	agcaatagcc	tactacgagg	ctaaggaggg	tatgctattc	420
gacagcctcc	tatataactc	aggtctgt				448

<210> 12

<211> 140

<212> PRT

<213> Artificial Sequence

<220>

<223> consensus sequence

<400> 12

Val	Lys	Thr	Leu	Ala	Leu	Ala	Gly	Ile	Ile	Ala	Ser	Ala	Ala	Leu	Ala	1	5	10	15
Leu	Leu	Ala	Gly	Phe	Ala	Thr	Thr	Gln	Ser	Pro	Leu	Ser	Phe	Tyr	Ala	20	25	30	
Thr	Gly	Thr	Ala	Gln	Ala	Val	Ser	Glu	Pro	Ile	Asp	Val	Glu	Ser	His	35	40	45	
Leu	Ser	Ile	Ala	Pro	Ala	Ala	Gly	Ala	Gln	Gly	Ser	Asp	Ile	Gly	Tyr	50	55	60	
Ile	Ile	Lys	Val	Asn	Val	Val	Lys	Leu	Lys	Val	Thr	Leu	Ala	Asn	Ala	65	70	75	80
Glu	Gln	Leu	Lys	Pro	Tyr	Phe	Lys	Tyr	Leu	Gln	Ile	Val	Leu	Ser	Ser	85	90	95	
Glu	Ile	Lys	Ala	Val	Ile	Ser	Leu	Asp	Lys	Pro	Ser	Ala	Val	Ile	Ile	100	105	110	
Leu	Asp	Glu	Asp	Phe	Ala	Ile	Ala	Tyr	Tyr	Glu	Ala	Lys	Glu	Gly	Met	115	120	125	
Leu	Phe	Asp	Ser	Leu	Pro	Val	Ile	Asn	Gln	Val	Leu					130	135	140	